REMARKS

The above amendatory action is taken to comply with the requirements of 37 CFR 1.821 - 1.825, as set forth in the Notice to filed Missing Parts mailed June 26, 2001 (copy attached). Applicants submit herewith the required statements that the paper copy and the computer readable form copy of the Sequence Listing are the same and contain no new matter.

Respectfully submitted,

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Figures 1A-1D illustrate [1a Illustration of] the step-wise procedure involved in analyses. The unknown biological material i.e. 'Adil.flesh' refers to the confiscated skin mentioned in 'Example 6'. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin `adil.flesh' was subjected to DNA isolation using the standard procedures[74]. The DNA obtained was amplified using the primers `mcb398' and `mcb869' in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane `M' shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from `adil.flesh' using primers `mcb398' and `mcb869'. The PCR amplicon obtained were sequenced at both the strand using "ABI Prism 3700 DNA Analyzes, PE-Applied Biosystems). The chromatogram shows the sequences (about 80 by long, i.e. between 150-230 by of sequence (328 bp), revealed from the PCR product of 472 by length) obtained from `adil.flesh'.

Figures 1E-1H illustrate [1b Illustrates] the further steps involved in *analyses*. The sequence (328 bp) revealed from `adil.flesh' was subjected to homology search in *nr* (i.e. non-redundant) database of Netional Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 by sequence from adil.flesh) and the sequences registered in *nr* database of NCBI. BLAST analysis revealed the highest homology of the sequence revealed from `adil.flesh' with the sequence of *Panthera pardus* (gene bank registration number `AY005809'), indicating the identity of adil.flesh as that of a leopard (*Panthera pardus*) origin.

Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from 'adil.flesh'. The sequences of `adil.flesh' is similar to the sequences of `gz1L' further confirming the identity of the source of confiscated remain `adil.flesh' as that of a *Panthera pardus* origin.

Figure[1c] 1I illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8)

from the sequences revealed from `adil.flesh' and reference animals listed in Table 5. The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. `adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard '*Panthera pardus*') indicating the identity of the species of `adil.flesh' as that of a *Panthera pardus* source.